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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=27; hr=14; min=5; sec=52; ms=114;]

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Application No: 10589180 Version No: 1.0

Input Set:

Output Set:

Started: 2008-08-23 06:13:30.047
Finished: 2008-08-23 06:13:33.279
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 232 ms
Total Warnings: 49
Total Errors: 0
No. of SeqIDs Defined: 54
Actual SeqID Count: 54

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W 213	Artificial or Unknown found in <213> in SEQ ID (4)
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Input Set:

Output Set:

Started: 2008-08-23 06:13:30.047
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Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 232 ms
Total Warnings: 49
Total Errors: 0
No. of SeqIDs Defined: 54
Actual SeqID Count: 54

Error code	Error Description
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SEQUENCE LISTING

<110> Merck & Co., Inc.
LaMonica, Nicola
Facciabene, Andrea
Aurisicchio, Luigi

<120> CARCINOEMBRYONIC ANTIGEN FUSIONS AND
USES THEREOF

<130> ITR0073YP

<140> 10589180
<141> 2008-08-23

<150> PCT/EP2005/001114
<151> 2005-02-03

<150> 60/635,791
<151> 2004-12-14

<150> 60/543,649
<151> 2004-02-11

<160> 54

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<213> Artificial Sequence

<220>
<223> PCR Primer, chemically synthesized

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<212> DNA
<213> Artificial Sequence

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<223> PCR Primer, chemically synthesized

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35

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<213> Artificial Sequence

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<223> PCR Primer, chemically synthesized

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tatgcggccg ctcataattc atcccgaatt ctgtt 35

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<223> CEA-LTA fusion

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acggcgttca atgtgcaga ggggaaggag gtgcTTCTAC ttgtccacaa tctgccccag 180
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ggatatgtaa taggaactca acaaGCTACC ccAGGGCCG catacagtgg tcgagagata 300
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accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggtta 420
tacccggagc tgcccaagcc ctccatctcc agcaacaact ccaaaccgt ggaggacaag 480

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 <211> 921
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA-LTB fusion

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 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
 35 40 45
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
 50 55 60

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
130 135 140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145 150 155 160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
165 170 175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
195 200 205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210 215 220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225 230 235 240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
245 250 255
Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
260 265 270
Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
275 280 285
Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
290 295 300
Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
305 310 315 320
Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
325 330 335
Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
340 345 350
Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
355 360 365
Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
370 375 380
Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
385 390 395 400
Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
405 410 415
Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
420 425 430
Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
435 440 445
Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
450 455 460
Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
465 470 475 480
Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
485 490 495
Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
500 505 510
Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln

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Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn		
545	550	555
Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser		
565	570	575
Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly		
580	585	590
Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly		
595	600	605
Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln		
610	615	620
Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu		
625	630	635
Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe		
645	650	655
Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile		
660	665	670
Thr Val Ser Ala Ser Gly Thr Leu Val Asn Gly Asp Lys Leu Tyr Arg		
675	680	685
Ala Asp Ser Arg Pro Pro Asp Glu Ile Lys Arg Ser Gly Gly Leu Met		
690	695	700
Pro Arg Gly His Asn Glu Tyr Phe Asp Arg Gly Thr Gln Met Asn Ile		
705	710	715
Asn Leu Tyr Asp His Ala Arg Gly Thr Gln Thr Gly Phe Val Arg Tyr		
725	730	735
Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser Leu Arg Ser Ala His Leu		
740	745	750
Ala Gly Gln Ser Ile Leu Ser Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val		
755	760	765
Ile Ala Thr Ala Pro Asn Met Phe Asn Val Asn Asp Val Leu Gly Val		
770	775	780
Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu Gly Gly Ile		
785	790	795
Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe Gly Val Ile		
805	810	815
Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg		
820	825	830
Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu Ala Gly Phe		
835	840	845
Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile His His Ala		
850	855	860
Pro Gln Gly Cys Gly Asn Ser Ser Arg Thr Ile Thr Asp Asp Thr Cys		
865	870	875
Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg Lys Tyr Gln		
885	890	895
Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser Glu Val Asp		
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Ile Tyr Asn Arg Ile Arg Asp Glu Leu		
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<211> 2355

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

<400> 9

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acgccgtca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
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<211> 784

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA-LTB fusion

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Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
35 40 45
Lys Glu Val Leu Leu Leu His Asn Leu Pro Gln His Leu Phe Gly
50 55 60
Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
65 70 75 80
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
85 90 95
Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
100 105 110
Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
115 120 125
Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
130 135 140
Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
145 150 155 160
Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
165 170 175
Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
180 185 190
Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
195 200 205
Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
210 215 220
Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
225 230 235 240
Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
245 25